

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Rao, Aragula Gururaj
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,392

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

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<160> 53

<170> FastSEQ for Windows Version 3.0

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<213> *Exophiala spinifera*

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attgtcgatc	gacgtcgatg	ctggtatctc	tggcaaatga	gatgggggtca	cagctcgatt	180
ggaggacgcc	cgagaagcct	tgctcgcgcc	accacggcct	gtcccatatc	aagactatct	240
tgctatagta	gcccaggata	gaattttccg	ccaatgcttg	cttctcggcg	ggaagagggtg	300
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<213> *Exophiala spinifera*

<400> 2

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 gatcgtagtg tacagccgga tgcgactgc tcaatttcag ccacgggggt gttgaggtgc 180
 ac 182

<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 3
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<210> 4
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<220>
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<400> 4
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<210> 5
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 <213> *Exophiala spinifera*

<220>
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc ctt 96
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt 144
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288

Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp		
				85					90						95		
ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	ccc	ttg	ctg	agc	gag	gag	336	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
			100					105				110					
ggt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
		115					120					125					
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	egg	432	
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
		130				135					140						
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480	
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150				155					160			
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	ggc	gct	ctg	ctc	ggt	528	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
			165					170					175				
gtg	gaa	goc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185					190				
agt	gcc	acc	ggt	ctc	agt	aat	att	tcc	tcg	gac	aag	aaa	gac	ggc	ggg	624	
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
		195				200						205					
cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672	
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
	210					215					220						
tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	720	
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225				230						235				240			
gaa	att	gag	cag	tcg	gca	ccc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
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gcc	gtg	tcc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	816	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260				265						270				
tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	864	
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
		275					280					285					
ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	912	
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
		290				295					300						
tcg	gac	aag	ccg	tcg	tcg	cgc	gaa	caa	ggc	tcc	tcg	ggc	gtc	ctc	caa	960	
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
305					310				315					320			

tgg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc 1008
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg 1056
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac 1104
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg 1152
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa gga 1200
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgg 1248
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 ccg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg 1296
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa 1344
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1386
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460
 tag 1389

<210> 6
 <211> 462
 <212> PRT
 <213> Exophiala spinifera

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
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Val	Ala	Ser	100	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	110	Gln	Leu	Ile
			115					120						125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
			130					135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
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Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
				165					170						175		
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185						190			
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
			195				200						205				
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
210						215						220					
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225					230						235				240		
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
				245					250						255		
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265						270			
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
			275				280						285				
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
290						295					300						
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
305					310					315					320		
Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val		
				325					330					335			
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg		
				340				345						350			
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp		
			355				360						365				
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro		
			370				375					380					
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly		
385					390						395				400		
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser		
				405				410						415			
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr		
			420					425						430			
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln		
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 <211> 1442
 <212> DNA
 <213> Exophiala spinifera

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<221> intron
 <222> (647)...(699)

<221> CDS

<222> (700) ... (1439)

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc gcc agg acg act atc aac gac ctc ggc gct ggc tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggg aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tgc gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g' gtgcgtgtgc' tgcgcgcaca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	

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210                215
tcgtttctca gtggctcattc cag gt atg cag tcg att tgc cat gcc atg tca      728
                Gly Met Gln Ser Ile Cys His Ala Met Ser
                        220                225

aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa      776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
                230                235                240

att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc      824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
                245                250                255

gtg ttc cga agc aaa aag gag gtg gtt tcg tta ccg aca acc ttg tat      872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
                260                265                270

ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg      920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
                275                280                285

gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg      968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
                290                295                300                305

gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg      1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
                310                315                320

agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat      1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
                325                330                335

cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag      1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
                340                345                350

tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa      1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
                355                360                365

ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc      1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
                370                375                380                385

aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct      1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
                390                395                400

ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg      1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
                405                410                415

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct      1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
                420                425                430

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ttt gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga 1400
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
 435 440 445

ggg gct gca gaa gtc gtg gct agc ctg gtc cca gca gca tag 1442
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 8
 <211> 462
 <212> PRT
 <213> *Exophiala spinifera*

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Cln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg


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          340          345          350
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
          355          360          365
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
          370          375          380
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
          385          390          395          400
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
          405          410          415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
          420          425          430
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 9
<211> 458
<212> PRT
<213> Exophiala spinifera

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
          35          40          45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
          50          55          60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
          65          70          75          80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
          85          90          95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
          100          105          110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
          115          120          125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
          130          135          140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
          145          150          155          160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
          165          170          175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
          180          185          190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
          195          200          205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
          210          215          220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
          225          230          235          240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
          245          250          255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
          260          265          270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
          275          280          285

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Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
290                295                300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305                310                315                320
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
                325                330                335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
                340                345                350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
                355                360                365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
                370                375                380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385                390                395                400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ile Ser Lys Glu
                405                410                425
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
                420                425                430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
                435                440                445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
450                455

```

```

<210> 10
<211> 1392
<212> DNA
<213> Exophiala spinifera

<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO

```

```

<400> 10
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
lys asp asn val ala asp val val val val gly ala gly leu ser gly
1                5                10                15

ctg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc      96
leu glu thr ala arg lys val gln ala ala gly leu ser cys leu val
                20                25                30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc      144
leu glu ala met asp arg val gly gly lys thr leu ser val gln ser
                35                40                45

ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      192
gly pro gly arg thr thr ile asn asp leu gly ala ala trp ile asn
                50                55                60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
asp ser asn gln ser glu val ser arg leu phe glu arg phe his leu
65                70                75                80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
10

```

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Gln His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ctg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac gcc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc gcc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
11	

```

305          310          315          320
caa tgc agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac 1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga 1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tcc gtc tgg 1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
          355          360          365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380

ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa 1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
          385          390          395          400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

tag 1392

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```

<210> 11
<211> 463
<212> PRT
<213> Exophiala spinifera

```

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<400> 11
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

```

```

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
      100      105      110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
      115      120      125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
      130      135      140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
      145      150      155      160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
      165      170      175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
      180      185      190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
      195      200      205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
      210      215      220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
      225      230      235      240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
      245      250      255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
      260      265      270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
      275      280      285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
      290      295      300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
      305      310      315      320
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
      325      330      335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
      340      345      350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
      355      360      365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
      370      375      380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
      385      390      395      400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
      405      410      415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
      420      425      430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
      435      440      445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
      450      455      460

```

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

<400> 12

ggggaattca aagacaaagt tgcggacgtg gtag

34

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23259

<400> 13

ggggcggcgc cctatgctgc tggcaccagg ctac

34

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14

tgggttcgtt accgacaacc ttgtatccc

29

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' race, N21968

<400> 15

gagttgggtcc cagacagact ttgttcgt

28

<210> 16

<211> 1673

<212> DNA

<213> Exophiala spinifera

<220>

<221> sig_peptide

<222> (1)...(267)

<223> yeast alpha mating factor secretion signal.

<221> CDS

<222> (1)...(1662)

<400> 16

atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc

48

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser

-85

-80

-75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa

96

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln

-70

-65

-60

```

att ccc gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc      144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
      -55                      -50                      -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg      192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
      -40                      -35                      -30

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta      240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
      -25                      -20                      -15                      -10

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg      288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                        -5                      1                      5

gac gtg gta gtg ggg ggc gct ggc ttg agc ggt ttg gag acg gca cgc      336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
      10                      15                      20

aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat      384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
      25                      30                      35

cgt gta ggg gga aag act ctg agc gta caa tgg ggt ccc ggc agg acg      432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
      40                      45                      50                      55

act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc      480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
      60                      65                      70

gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag      528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
      75                      80                      85

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act      576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
      90                      95                      100

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca      624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
      105                      110                      115

ctc gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc      672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
      120                      125                      130                      135

ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg      720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
      140                      145                      150

agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc      768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
      155                      160                      165

ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac      816
      15

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Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	364
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	
ctc agt aat att ttc tcc gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcc att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca gcc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcc gca tcc gcc tgt aca gta cga tcc gcc tcc gcc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcc tta ccc aca acc ttc tat ccc acc ttc	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttc ggc gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg gcc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa gcc ttc tcc gcc gtc ctc caa tcc agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
315 320 325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
330 335 340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
345 350 355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
360 365 370 375	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
380 385 390	
gaa atc gag tgg tcc aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	


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gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg      1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
      410                      415                      420

ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg      1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
      425                      430                      435

aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca      1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
      440                      445                      450                      455

gaa gtt gtg gct agc ctg gtg cca gca gca tagggcgccg c      1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala
      460                      465

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<210> 17
<211> 554
<212> PRT
<213> Exophiala spinifera

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<220>
<221> SIGNAL
<222> (1)...(89)

```

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<400> 17
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
      -85                      -80                      -75
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
      -70                      -65                      -60
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
      -55                      -50                      -45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
      -40                      -35                      -30
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
      -25                      -20                      -15                      -10
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
      -5                      -1                      5
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
      10                      15                      20
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
      25                      30                      35
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
      40                      45                      50                      55
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
      60                      65                      70
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
      75                      80                      85
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
      90                      95                      100
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
      105                      110                      115
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
      120                      125                      130                      135
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
      140                      145                      150

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```

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
      155      160      165
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
      170      175      180
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
      185      190      195
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
200      205      210      215
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
      220      225      230
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
      235      240      245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
      250      255      260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
      265      270      275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280      285      290      295
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
      300      305      310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
      315      320      325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
      330      335      340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
      345      350      355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360      365      370      375
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
      380      385      390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
      395      400      405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
      410      415      420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
      425      430      435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440      445      450      455
Glu Val Val Ala Ser Leu Val Pro Ala Ala
      460      465

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<210> 18
 <211> 2079
 <212> DNA
 <213> Unknown

<220>
 <223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<221> CDS
 <222> (1)...(2076)

<221> misc_feature
 <222> (1)...(687)

<223> gst fusion + polylinker

<221> misc_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc_feature

<222> (688)...(690)

<223> Extra lysine

<400> 18

```

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc      48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1              5              10              15

acc cga cct ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
              20              25              30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
              35              40              45

ggg ttg gag ttt ccc aac cct cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
  50              55              60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
  65              70              75              80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
              85              90              95

gga gcg gtt ttg gat att aga tac ggt gtt tgg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
  100              105              110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
  115              120              125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
  130              135              140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
  145              150              155              160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
              165              170              175

gtt tgt ttt aaa aaa cgt att gaa gct atc oca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
  180              185              190

```

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tgg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly 225 230 235 240	720
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245 250 255	768
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 260 265 270	816
ctg agc gta caa tgg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tgg 20	1296

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tgc att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc tca ttc gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgc aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	
ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg 2016
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670

gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg 2064
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685

gtg cca gca gca tag 2079
 Val Pro Ala Ala
 690

<210> 19
 <211> 692
 <212> PRT
 <213> Unknown

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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525
 Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685
 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <223> Nucleotide sequence of K:trAPAO translational

fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464, trAPAO cDNA.

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

<221> CDS
<222> (1)...(1461)

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

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-20 -15 -10	
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta	96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val	
-5 1 5	
gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag	144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	
10 15 20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg	192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
25 30 35 40	
gga aag act ctg agc gta caa tgc ggt ccc gcc agg acg act atc aac	240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
45 50 55	
gac ctc gcc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc	288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
60 65 70	
aga ttg ttc gaa aga ttc cat ttg gag gcc gag ctc cag agg acg act	336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	
75 80 85	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct	384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	
90 95 100	
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctc gcg gaa	432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	
105 110 115 120	


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ctc ctc ccc gta cgg cct cag ctg atc gaa gag cat agc ctt caa gac      480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
125                               130                               135

ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg      528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
140                               145                               150

cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca      576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
155                               160                               165

aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc      624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
170                               175                               180

atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat      672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185                               190                               195                               200

att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca      720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
205                               210                               215

ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc      768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
220                               225                               230

tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc      816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
235                               240                               245

ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag      864
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
250                               255                               260

gtg gtg gct tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca      912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265                               270                               275                               280

cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg      960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
285                               290                               295

ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc     1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
300                               305                               310

gaa caa gcc ttc tcg gcc gtc ctc caa tcg agc tgt gac ccc atc tca     1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
315                               320                               325

ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc     1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
330                               335                               340

tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag     1152
25

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Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
 345 350 355 360
 cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag 1200
 Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
 365 370 375
 aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtc ctc gaa atc gag 1248
 Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
 380 385 390
 tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg 1296
 Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
 395 400 405
 ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag 1344
 Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
 410 415 420
 agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat 1392
 Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
 425 430 435 440
 atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg 1440
 Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
 445 450 455
 gcc agc ctg gtg cca gca gca tag 1464
 Ala Ser Leu Val Pro Ala Ala
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<210> 21
 <211> 487
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

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 -5 1 5
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
 10 15 20
 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
 25 30 35 40
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
 45 50 55
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
 60 65 70
 Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
 75 80 85
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro

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      90              95              100
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105              110              115              120
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
      125              130              135
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
      140              145              150
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
      155              160              165
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
      170              175              180
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185              190              195              200
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
      205              210              215
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
      220              225              230
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
      235              240              245
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
      250              255              260
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265              270              275              280
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
      285              290              295
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
      300              305              310
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
      315              320              325
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
      330              335              340
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345              350              355              360
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
      365              370              375
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
      380              385              390
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
      395              400              405
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
410              415              420
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
425              430              435              440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
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Ala Ser Leu Val Pro Ala Ala
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<210> 22
<211> 1803
<212> DNA
<213> Exophiala spinifera

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<220>
<221> CDS
<222> (1)...(1800)

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<400> 22

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1 5 10 15	
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tgc ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tgc gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	
195 200 205	
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
28	

225	230	235	240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg				768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala				
	245	250	255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa				816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln				
	260	265	270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc				864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				
	275	280	285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta				912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val				
	290	295	300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc				960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile				
	305	310	315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt				1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				
	325	330	335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa				1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				
	340	345	350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca				1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				
	355	360	365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca				1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala				
	370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa				1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				
	385	390	395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt				1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				
	405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc				1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile				
	420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg				1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp				
	435	440	445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc				1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				
	450	455	460	

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tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att 1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                               470                               475                               480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc 1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                               485                               490                               495

aag cag gta cga caa aag tct gtc tgg gac cca ctc cgc gca gcc tac 1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                               500                               505                               510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
                               515                               520                               525

gag tgg tgg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
                               530                               535                               540

ggg ctg aac gat ctc atc aca ctg ggt tgg gcg ctc aga acg ccg ttc 1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                               550                               555                               560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                               565                               570                               575

tat atg gaa ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt 1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
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gtg gct agc ctg gtg cca gca gca tag 1803
Val Ala Ser Leu Val Pro Ala Ala
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<211> 600
<212> PRT
<213> Exophiala spinifera

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20     25     30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35     40     45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50     55     60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65     70     75     80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85     90     95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100    105    110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
30

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115	120	125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
180	185	190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
195	200	205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
210	215	220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala		
225	230	235
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
260	265	270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
275	280	285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
290	295	300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile		
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		
325	330	335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
340	345	350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
355	360	365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
370	375	380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		
385	390	395
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		
405	410	415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
450	455	460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
465	470	475
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
485	490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
500	505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
565	570	575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		

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 Val Ala Ser Leu Val Pro Ala Ala
 595 600

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 <212> DNA
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 esp1 mat: an artificial spacer sequence and
 K:trAPAO

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 -20 -15 -10
 ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
 -5 1 5
 ggg atg gtg gtc gcc acg act act act gtc ccc gcc acc act ggc acc 144
 Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 gtc agc gag ttc ttg gcc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40
 ggc cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55

gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu 60 65 70	288
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly 75 80 85	336
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 90 95 100	384
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 105 110 115 120	432
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 125 130 135	480
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 140 145 150	528
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 155 160 165	576
ttc cta gac caa agg ttc gct ttg gat tgg gta cag ccg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 170 175 180	624
gcc ttc gcc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 185 190 195 200	672
ggg gcc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 205 210 215	720
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 220 225 230	768
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 235 240 245	816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 250 255 260	864
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttc gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 265 270 275 280	912
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
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aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	
315 320 325	
ctc gag gag gca atc cgg aat cag ccc gac ctt tac cag acc ctc ctt	1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu	
330 335 340	
gga gca tat ccc att gga tcc cca ggg atc gga tgg cct caa gat cag	1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln	
345 350 355 360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc	1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
365 370 375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac	1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
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tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg	1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val	
395 400 405	
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Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala	
410 415 420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc	1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala	
425 430 435 440	
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa	1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln	
445 450 455	
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Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val	
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Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg	
475 480 485	
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Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly	
490 495 500	
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Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val	
505 510 515 520	

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act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
ccr tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc gcc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tgc gac aag aaa gac gcc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tgc att tgc cat gcc atg tca aag gaa ctt gct cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tgc gca	2352

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
745 750 755 760	
tcc gcc tgt aca gta cga tgc gcc tgc gcc gtc ttc cga agc aaa	2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
765 770 775	
aag gtg gtg gtt tgc tca ccg aca acc ttg tat ccc acc ttg aca ttc	2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
780 785 790	
tca cca cct ctg ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
795 800 805	
ctg gcc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	2544
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810 815 820	
cgc gaa caa gcc ttc tgc gcc gtc ctg caa tgc agc tgt gac ccc atc	2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
825 830 835 840	
tca ttc gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
845 850 855	
acc tgt ttc atg gtc gga gac ccg gga ccg aag tgg tcc caa cag tcc	2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
860 865 870	
aag cag gta cga caa aag tct gtc tgg gac caa ctg cgc gca gcc tac	2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
875 880 885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctg gaa atc	2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
890 895 900	
gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
905 910 915 920	
ggg ctg aac gat ctg atc aca ctg ggt tgc gcg ctg aga acg ccg ttc	2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
925 930 935	
aag agt gtt cat ttc gtt gga acg gag acg tct tca gtt tgg aaa ggg	2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
940 945 950	
tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt	2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
955 960 965	
gtg gct agc ctg gtg cca gca gca tag	3003
Val Ala Ser Leu Val Pro Ala Ala	

970

975

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 <221> SIGNAL
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<400> 25

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Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
			-5									5			
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
	10				15						20				
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe
	25				30				35					40	
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr
			45					50					55		
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu
			60					65					70		
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly
	75					80					85				
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu
	90				95						100				
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu
	105				110					115				120	
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala
			125						130				135		
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu
			140					145					150		
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly
	155					160					165				
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala
	170					175				180					
Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala
	185				190					195				200	
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro
			205						210				215		
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe
			220					225					230		
Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu
	235					240						245			
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp
	250				255					260					
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu
	265				270					275				280	
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg
			285						290				295		
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala
			300					305					310		
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr
	315						320					325			
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu

37

330		335		340
Gly Ala Tyr Pro Ile	Gly Ser Pro Gly Ile	Gly Ser Pro Gln Asp Gln		
345	350	355		360
Ile Ala Ala Ile Glu Thr	Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
	365	370		375
Val Ala Gln Asp Ser Arg Asn Arg	Gly Ile Pro Ser Trp Arg Tyr Tyr			
	380	385		390
Tyr Asn Ala Thr Phe Glu Asn Leu	Glu Leu Phe Pro Gly Ser Glu Val			
	395	400		405
Tyr His Ser Ser Glu Val	Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
	410	415		420
Ser Ala Thr Ala Leu Glu Ala Gln Thr	Ser Lys Tyr Met Gln Gly Ala			
	425	430		435
Trp Ala Ala Phe Ala Lys Asn Pro Met	Asn Gly Pro Gly Trp Lys Gln			
	445	450		455
Val Pro Asn Val Ala Ala Leu Gly	Ser Pro Gly Lys Ala Ile Gln Val			
	460	465		470
Asp Val Ser Pro Ala Thr Ile	Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
	475	480		485
Tyr Tyr Thr Glu Leu Gly Thr Ile	Ala Pro Arg Thr Phe Gly Gly Gly			
	490	495		500
Ser Gly Gly Gly Ser Gly Gly Gly	Ser Lys Asp Asn Val Ala Asp Val			
	505	510		515
Val Val Val Gly Ala Gly Leu Ser	Gly Leu Glu Thr Ala Arg Lys Val			
	525	530		535
Gln Ala Ala Gly Leu Ser Cys Leu	Val Leu Glu Ala Met Asp Arg Val			
	540	545		550
Gly Gly Lys Thr Leu Ser Val Gln	Ser Gly Pro Gly Arg Thr Thr Ile			
	555	560		565
Asn Asp Leu Gly Ala Ala Trp	Ile Asn Asp Ser Asn Gln Ser Glu Val			
	570	575		580
Ser Arg Leu Phe Glu Arg Phe His	Leu Glu Gly Glu Leu Gln Arg Thr			
	585	590		595
Thr Gly Asn Ser Ile His Gln	Ala Gln Asp Gly Thr Thr Thr Ala			
	605	610		615
Pro Tyr Gly Asp Ser Leu Leu Ser	Glu Glu Val Ala Ser Ala Leu Ala			
	620	625		630
Glu Leu Leu Pro Val Trp Ser Gln	Leu Ile Glu Glu His Ser Leu Gln			
	635	640		645
Asp Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp Ser Val Ser Phe			
	650	655		660
Ala His Tyr Cys Glu Lys Glu	Leu Asn Leu Pro Ala Val Leu Gly Val			
	665	670		675
Ala Asn Gln Ile Thr Arg Ala	Leu Leu Gly Val Glu Ala His Glu Ile			
	685	690		695
Ser Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly Leu Ser			
	700	705		710
Asn Ile Phe Ser Asp Lys Lys	Asp Gly Gly Gln Tyr Met Arg Cys Lys			
	715	720		725
Thr Gly Met Gln Ser Ile Cys	His Ala Met Ser Lys Glu Leu Val Pro			
	730	735		740
Gly Ser Val His Leu Asn Thr	Pro Val Ala Glu Ile Glu Gln Ser Ala			
	745	750		755
Ser Gly Cys Thr Val Arg Ser	Ala Ser Gly Ala Val Phe Arg Ser Lys			
	765	770		775
Lys Val Val Val Ser Leu	Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
	780	785		790
Ser Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			

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      795                      800                      805
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
  810                      815                      820
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
  825                      830                      835                      840
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
      845                      850                      855
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      860                      865                      870
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
      875                      880                      885
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
      890                      895                      900
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
  905                      910                      915                      920
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
      925                      930                      935
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
      940                      945                      950
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
      955                      960                      965
Val Ala Ser Leu Val Pro Ala Ala
  970                      975

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<210> 26
<211> 2976
<212> DNA
<213> Unknown

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<220>
<223> Barley alpha amylase signal sequence: BEST1
      mature: artificial spacer: and K:trAPAO. For
      plant expression.

```

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<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

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<221> mat_peptide
<222> (73)...(1545)
<223> BEST1 mature

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<221> misc_feature
<222> (1546)...(1584)
<223> spacer sequence

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<221> misc_feature
<222> (1585)...(2973)
<223> K:trAPAO

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<221> CDS
<222> (1)...(2973)

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<221> misc_feature
<222> (1585)...(1587)
<223> Extra lysine

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<400> 26
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 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10

ctc tcc gcc tcc ctc gcc agc gcc acg gat ttt ccg gtc cgc agg acc 96
 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
 -5 1 5

gat ctg gcc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
 10 15 20

gga ata ccc tat gca gcg ccg ccg gtg gcc ggg ctg cgt tgg aag ccg 192
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
 25 30 35 40

ccc caa cac gcc cgg ccc tgg gcg gcc gtt cgc ccc gcc acc caa ttt 240
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
 45 50 55

ggc tcc gac tgc ttc gcc gcg gcc tat ctt cgc aaa gcc agc ctc gcc 288
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
 60 65 70

ccc gcc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
 75 80 85

ggc gct aaa ccc gcc cag tac ccc gtc atg gtc tgg gtc tac gcc gcc 384
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
 90 95 100

ggc ttc gcc gcc gcc acg gcc gcc atg ccc tac tac gac gcc gag gcg 432
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
 105 110 115 120

ctt gcg cga cag gcc gtc gtc gtg gtg acg ttt aac tat cgg acg aac 480
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
 125 130 135

atc ctg gcc ttt ttc gcc cat cct ggt ctc tcc cgc gag agc ccc acc 528
 Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
 140 145 150

gga acc tcc gcc aac tac gcc cta ctc gac att ctc gcc gct ctt cgg 576
 Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
 155 160 165

tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc gcc cga gtg 624
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
 170 175 180

acg gtc ttt ggt gaa tcc gcc gga gcg agc gcc atc gga ctt ctg ctc 672
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
 185 190 195 200

acc tgc ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt	720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	
205 210 215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tgc	768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	
220 225 230	
ggc gag cgc ctc gac gcc gat ctt tgc cga ctg cgc tgc acc gac cca	816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
235 240 245	
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tgc cgg gac	864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
250 255 260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg	912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	
265 270 275 280	
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt	960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	
285 290 295	
egg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg	1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	
300 305 310	
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg	1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	
315 320 325	
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac	1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp	
330 335 340	
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat	1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	
345 350 355 360	
cag ttc aat cgg ggg gtc tgc gcc ttc tgc gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acc ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc cgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	

425	430	435	440	
egg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct				1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro				
	445	450	455	
gcc tat tct acg ggc aag tgc acc atg aca ttc ggt ccc gag ggc cgc				1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg				
	460	465	470	
gcg gcg gtg gtg tgc ccc gga cct tcc atc ccc cct tgc gcg gat ggc				1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly				
	475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc				1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser				
	490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt				1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				
	505	510	515	520
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc				1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val				
	525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc				1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
	540	545	550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat				1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
	555	560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg				1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
	570	575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
	585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
	605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
	620	625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
	635	640	645	
egg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac				2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
	650	655	660	

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ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc      2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                      670                      675                      680

ggg ggg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                      685                      690                      695

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac gcc      2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                      700                      705                      710

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
                      715                      720                      725

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                      735                      740

gct gaa att gag cag tcg gca tcc gcc tgt aca gta cga tcg gcc tcg      2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                      750                      755                      760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                      765                      770                      775

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
780                      785                      790

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                      800                      805

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc      2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                      815                      820

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac      2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga      2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845                      850                      855

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                      865                      870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                      880                      885

ccg gcc aac ggg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa      2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln

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890	895	900	
gga gct cgc agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
905	910	915	920
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
	925	930	935
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
	940	945	950
caa cga ggt gct gca gaa gtt gtg gcc agc ctg gtg cca gca gca			2973
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
	955	960	965
tag			2976

<210> 27
 <211> 991
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

<400> 27

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Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr
			-5				1					5			
Asp	Leu	Gly	Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg
	10				15					20					
Gly	Ile	Pro	Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro
	25			30					35					40	
Pro	Gln	His	Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe
			45					50						55	
Gly	Ser	Asp	Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala
			60					65					70		
Pro	Gly	Val	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser
		75				80					85				
Gly	Ala	Lys	Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly
	90				95						100				
Gly	Phe	Ala	Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala
	105				110					115				120	
Leu	Ala	Arg	Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn
			125						130					135	
Ile	Leu	Gly	Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr
			140					145					150		
Gly	Thr	Ser	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg
		155				160					165				
Trp	Val	Gln	Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val
	170					175					180				
Trp	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu
	185					190				195					200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
 205 210 215
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
 220 225 230
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
 235 240 245
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
 250 255 260
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
 265 270 275 280
 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
 285 290 295
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
 300 305 310
 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
 315 320 325
 Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
 330 335 340
 Gly Arg Ala Thr Pro Lys Gly Met Val Ala Arg Ile Phe Gly Asp Asn
 345 350 355 360
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
 365 370 375
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
 380 385 390
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
 410 415 420
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
 425 430 435 440
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
 445 450 455
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
 460 465 470
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
 475 480 485
 Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 490 495 500
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 505 510 515 520
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 525 530 535
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 540 545 550
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 555 560 565
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 570 575 580
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 585 590 595 600
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Gln
 605 610 615
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 620 625 630
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 635 640 645
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 650 655 660

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Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
565                               570                               575                               580
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                               585                               590                               595
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                               700                               705                               710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
                               715                               720                               725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                               735                               740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                               750                               755                               760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                               765                               770                               775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                               780                               785                               790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                               800                               805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                               815                               820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                               830                               835                               840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                               845                               850                               855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                               865                               870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                               880                               885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890                               895                               900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                               910                               915                               920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                               925                               930                               935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940                               945                               950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955                               960                               965

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<210> 28
 <211> 3618
 <212> DNA
 <213> Unknown

<220>
 <223> gst:espl:sp:K:trapao, 3618. 1-687, gst +
 polylinker; 688-2190, espl mat; 2191-2226 spacer;
 2227-3615, K:trAPAO, 3616-3618, stop codon. For
 bacterial expression.

<221> CDS
 <222> (1)...(3615)
 <221> misc_feature
 <222> (1)...(687)
 <223> ~~gst + polylinker~~

<221> mat_peptide
 <222> (688)...(2190)
 <223> espi mat

<221> misc_feature
 <222> (2191)...(2226)
 <223> spacer sequence

<221> misc_feature
 <222> (2227)...(3615)
 <223> K:trAPO

<221> misc_feature
 <222> (2227)...(2229)
 <223> Extra lysine

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 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

gga gcg gtt ttg gat att aga tac ggt gtt tgg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

gtt gtt tta tac atg gac cca atg tgc cgc gat gcg ttc cca aaa tta 528

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcc gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg	720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
gtc gcc acg act act act gtc ccc gcc acc act gcg acc gtc agc gag	768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
245 250 255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct	816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
260 265 270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt	864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
275 280 285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctg cgt gag att	912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
290 295 300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag	960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	
305 310 315 320	
gac tgc ctg aac ctg aac atc tac gtc cca gga act gag aac aca aac	1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
325 330 335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg	1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
340 345 350	
aat tca ttc cac ctg tac gac ggg gct agt ttc gca gcc aat cag gat	1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	
355 360 365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct	1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
370 375 380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
385 390 395 400	

caa agg tct gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggc gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg 435 440 445	1344
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460	1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510	1536
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gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545 550 555 560	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575	1728
ccc att gga tcc cca ggg atc gga tgc cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc 49	1920

Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640	
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655	1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670	2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675 680 685	2064
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly 725 730 735	2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592

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ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag      2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
865                      870                      875                      880

gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac      2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
885                      890                      895

tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag      2736
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
900                      905                      910

atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctc      2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
915                      920                      925

ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc      2832
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
930                      935                      940

tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg      2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
945                      950                      955                      960

cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg      2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
965                      970                      975

cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt      2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
980                      985                      990

aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg      3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
995                      1000                      1005

gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct      3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
1010                      1015                      1020

ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac      3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr
1025                      1030                      1035                      1040

tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa      3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
1045                      1050                      1055

ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc      3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
1060                      1065                      1070

aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc      3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe
1075                      1080                      1085

atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta      3312

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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
 1090 1095 1100

cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc 3360
 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
 1105 1110 1115 1120

ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgg 3408
 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
 1125 1130 1135

aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ccg aac 3456
 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
 1140 1145 1150

gat ctc atc aca ctg ggt tgg ggc ctc aga acg ccg ttc aag agt gtt 3504
 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
 1155 1160 1165

cat ttc gtc gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa 3552
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
 1170 1175 1180

ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
 1185 1190 1195 1200

ctg gtg cca gca gca tag 3618
 Leu Val Pro Ala Ala
 1205

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
      225      230      235      240
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
      245      250      255
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
      260      265      270
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
      275      280      285
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
      290      295      300
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
      305      310      315      320
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
      325      330      335
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
      340      345      350
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
      355      360      365
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
      370      375      380
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
      385      390      395      400
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
      405      410      415
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
      420      425      430
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
      435      440      445
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
      450      455      460
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
      465      470      475      480
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr
      485      490      495
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu
      500      505      510
Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly
      515      520      525
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
      530      535      540
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu
      545      550      555      560
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr
      565      570      575
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
      580      585      590
Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln
      595      600      605
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
      610      615      620

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Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser
 625 630 635 640
 Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr
 645 650 655
 Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala
 660 665 670
 Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn
 675 680 685
 Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser
 690 695 700
 Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr
 705 710 715 720
 Gln Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly
 725 730 735
 Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val
 740 745 750
 Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala
 755 760 765
 Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys
 770 775 780
 Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu
 785 790 795 800
 Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu
 805 810 815
 Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn
 820 825 830
 Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly
 835 840 845
 Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
 850 855 860
 Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
 865 870 875 880
 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
 885 890 895
 Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
 900 905 910
 Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
 915 920 925
 Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
 930 935 940
 Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
 945 950 955 960
 Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
 965 970 975
 His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
 980 985 990
 Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
 995 1000 1005
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
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 1025 1030 1035 1040
 Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
 1045 1050 1055
 Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
 1060 1065 1070
 Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe
 1075 1080 1085

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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
1090                      1095                      1100
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
1105                      1110                      1115                      1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
                      1125                      1130                      1135
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
                      1140                      1145                      1150
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
                      1155                      1160                      1165
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
1170                      1175                      1180
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Leu Val Pro Ala Ala
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<212> DNA
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bacterial expression vector pGEX-4T-1 or similar
vector. gst: BEST1:sp:K:trAPAO fusion, 3591 nt.
1-687 gst
+ polylinker, 688-2163, BEST1 mature; 2164-2199,
spacer, 2200-3588, K:trAPAO

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1                      5                      10                      15

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55

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30	96
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45	144
ggc ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60	192
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80	240
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95	288
gga gcg gtc ttg gat att aga tac ggt gtt tgc aga att gca tat agt Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110	336
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125	384
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140	432
ggc gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160	480
gtc gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175	528
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190	576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag gcc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tgc gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly 225 230 235 240	720
cag gtc cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc 56	768

Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
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 Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
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 gcc cgg ccc tgg gcg ggc gtc cgc ccc gcc acc caa ttt ggc tcc gac 864
 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
 275 280 285
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 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
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 agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa 960
 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
 305 310 315 320
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 325 330 335
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 Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
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 cag gcc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc 1104
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 355 360 365
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 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
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 ggc aac tac gcc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag 1200
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
 385 390 395 400
 agc aac gcc cgc gcc ttc gga ggg gac ccc gcc cga gtg acg gtc ttt 1248
 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
 405 410 415
 ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg 1296
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
 420 425 430
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 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
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 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
 450 455 460
 ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac coa gcc acc ctg 1440
 Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
 465 470 475 480

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ccg cgt ccg acc gga ccg atc gtc gat gcc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510	1536
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu 515 520 525	1584
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atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt gcc Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly 545 550 555 560	1680
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac gcc cgg gcc Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala 565 570 575	1728
acg ccc aag gaa atg gtc gcg cgc atc ttc gcc gac aat cag ttc aat Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn 580 585 590	1776
cgg ggg gtc tgc gcc ttc tgc gaa gcg ctt gtg cgc cag gcc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605	1824
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro 610 615 620	1872
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625 630 635 640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645 650 655	1968
gac cgt gcg ctg gcc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala 660 665 670	2016
aag aat gcc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675 680 685	2064
acg gcc aag tgc acc atg aca ttc ggt ccc gag gcc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 690 695 700	2112
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Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala		
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gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	acg	2256	
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gca	cgc	aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	2304	
Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala		
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Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly		
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agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	2400	
Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn		
785					790					795					800		
caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	2448	
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu		
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ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggg	aca	2496	
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr		
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acc	act	aca	gct	cct	tat	ggg	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	2544	
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala		
			835				840					845					
agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	2592	
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu		
	850					855					860						
cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gag	aag	cgg	ctc	gac	2640	
His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp		
	865				870				875					880			
agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	2688	
Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala		
			885					890					895				
gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggg	gtg	gaa	2736	
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gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	2784	
Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala		
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acc	ggg	ctc	agt	aat	att	ttc	tgc	gac	aag	aaa	gac	ggc	ggg	cag	tat	2832	
Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr		
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gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att      2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
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gag cag tgc gca tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg      2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
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ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc      3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
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acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg      3072
Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
1010                      1015                      1020

gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac      3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
1025                      1030                      1035                      1040

aag ccg tgg tgg cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc      3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
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tgt gac ccc atc tca ttc gcc aga gat acc agc atc gac gtc gat cga      3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
1060                      1065                      1070

caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg      3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
1075                      1080                      1085

tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc      3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
1090                      1095                      1100

cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac      3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
1105                      1110                      1115                      1120

gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct ccg      3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
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agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc      3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
1140                      1145                      1150

aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta      3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
1155                      1160                      1165

gct tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt      3552

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3591

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35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
225 230 235 240
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
245 250 255
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
260 265 270
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
275 280 285
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
290 295 300
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
305 310 315 320
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
325 330 335
~~Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg~~
340 345 350

Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
 355 360 365
 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
 370 375 380
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
 385 390 395 400
 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
 405 410 415
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
 420 425 430
 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
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 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
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 465 470 475 480
 Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
 485 490 495
 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
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 Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
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 545 550 555 560
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 Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn
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 595 600 605
 Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro
 610 615 620
 Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu
 625 630 635 640
 Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala
 645 650 655
 Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
 660 665 670
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 675 680 685
 Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
 690 695 700
 Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala
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 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Lys Asp Asn
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 Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr
 740 745 750
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 Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly
 770 775 780
 Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn
 785 790 795 800
 Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu
 805 810 815

Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
 820 825 830
 Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Val Ala
 835 840 845
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
 850 855 860
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
 865 870 875 880
 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
 885 890 895
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
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 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
 915 920 925
 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
 930 935 940
 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
 945 950 955 960
 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
 965 970 975
 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
 980 985 990
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
 995 1000 1005
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 Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
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 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
 1125 1130 1135
 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
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 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
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glycosylation sites

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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
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aca ata gct gga cag att gga caa gac gct tcc ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
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ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
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tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
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Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
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Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	

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 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 66

	85		90		95
Leu Lys Ala Thr	Phe Ala Leu Asp Arg	Leu Pro Pro Cys Thr	Leu Val		
100	105	110			
Pro Val Ser Ala	Leu Ser Ser Pro Glu Tyr	Leu Phe Glu Val	Asp Ala		
115	120	125			
Thr Ala Leu Val	Pro Gly His Thr Thr	Pro Asp Asn Val	Ala Asp Val		
130	135	140			
Val Val Val Gly	Ala Gly Leu Ser Gly	Leu Glu Thr	Ala Arg Lys Val		
145	150	155	160		
Gln Ala Ala Gly	Leu Ser Cys Leu Val	Leu Glu Ala	Met Asp Arg Val		
165	170	175			
Gly Gly Lys Thr	Leu Ser Val Gln Ser Gly	Pro Gly Arg Thr	Thr Thr Ile		
180	185	190			
Asn Asp Leu Gly	Ala Ala Trp Ile Asn Asp	Ser Asn Gln	Ala Glu Val		
195	200	205			
Ser Arg Leu Phe	Glu Arg Phe His Leu	Glu Gly Glu Leu	Gln Arg Thr		
210	215	220			
Thr Gly Asn Ser	Ile His Gln Ala	Gln Asp Gly Thr	Thr Thr Thr	Ala	
225	230	235	240		
Pro Tyr Gly Asp	Ser Leu Leu Ser Glu	Glu Val Ala Ser	Ala Leu Ala		
245	250	255			
Glu Leu Leu Pro	Val Trp Ser Gln Leu	Ile Glu Glu His	Ser Leu Gln		
260	265	270			
Asp Leu Lys Ala	Ser Pro Gln Ala Lys	Arg Leu Asp Ser	Val Ser Phe		
275	280	285			
Ala His Tyr Cys	Glu Lys Glu Leu Asn	Leu Pro Ala Val	Leu Gly Val		
290	295	300			
Ala Asn Gln Ile	Thr Arg Ala Leu Leu	Gly Val Glu Ala	His Glu Ile		
305	310	315	320		
Ser Met Leu Phe	Leu Thr Asp Tyr Ile	Lys Ser Ala Thr	Gly Leu Ser		
325	330	335			
Asn Ile Phe Ser	Asp Lys Lys Asp Gly	Gly Gln Tyr Met	Arg Cys Lys		
340	345	350			
Thr Gly Met Gln	Ser Ile Cys His Ala	Met Ser Lys Glu	Leu Val Pro		
355	360	365			
Gly Ser Val His	Leu Asn Thr Pro Val	Ala Glu Ile Glu	Gln Ser Ala		
370	375	380			
Ser Gly Cys Thr	Val Arg Ser Ala Ser	Gly Ala Val Phe	Arg Ser Lys		
385	390	395	400		
Lys Val Val Val	Ser Leu Pro Thr Thr	Leu Tyr Pro Thr	Leu Thr Phe		
405	410	415			
Ser Pro Pro Leu	Pro Ala Glu Lys Gln	Ala Leu Ala Glu	Asn Ser Ile		
420	425	430			
Leu Gly Tyr Tyr	Ser Lys Ile Val Phe	Val Trp Asp Lys	Pro Trp Trp		
435	440	445			
Arg Glu Gln Gly	Phe Ser Gly Val	Leu Gln Ser Ser	Cys Asp Pro	Ile	
450	455	460			
Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val Asp Arg Gln	Trp Ser Ile		
465	470	475	480		
Thr Cys Phe Met	Val Gly Asp Pro Gly	Arg Lys Trp Ser	Gln Gln Ser		
485	490	495			
Lys Gln Val Arg	Gln Lys Ser Val Trp	Asp Gln Leu Arg	Ala Ala Tyr		
500	505	510			
Glu Asn Ala Gly	Ala Gln Val Pro Glu	Pro Ala Asn Val	Leu Glu Ile		
515	520	525			
Glu Trp Ser Lys	Gln Gln Tyr Phe Gln	Gly Ala Pro Ser	Ala Val Tyr		
530	535	540			
Gly Leu Asn Asp	Leu Ile Thr Leu	Gly Ser Ala Leu	Arg Thr Pro	Phe	

545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Glu Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 34
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 37-mer oligonucleotide

<400> 34
 ggggaattca tggcacttgc accgagctac atcaatc

37

<210> 35
 <211> 1929
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 35
 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc aggggtattcc 60
 cacatcgggc tagggccaaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
 gacgctttcg gcgtgacaga cccagcctac gagaaacagg ttgcccacgc attcgccaat 180
 ctgcgagctt gccttgctgc agttggagcc tcctcaaacy acgtcaccaa gctcaattac 240
 tacatcgctg actacgcccc gagcaaaact accgcaattg gagatgggct gaagtctacc 300
 tttgcccttg acaggctccc tcccttgacg ctggtgcccag taccggcctt ggcttcacct 360
 gaatacctct ttgaggttga tgccacggcg ctggtgcccag gacactcgac cccagacaa 420
 gttagcgagc tggtagtggt gggcgctggc ttgagcggtt tggagacggc accgaaagtc 480
 caggccgcgc gctgttctcg cctcgctctt gaggcgatgg atcgtgtagg gggaaagact 540
 ctgagcgtac aatcggttcc cggcaggacg actatcaacg acctcgggcg tgcgtggatc 600
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggaggggcag 660
 ctccagagga cgaccggaaa ttcaatccat caagcacaaag accgtacacac cactacagct 720
 cottatgggtg actcccccgt aagcacaaat ccactctgtg atgagacctc tctcgaggtg 780
 agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcac gtgcacttgc 840
 ggaactcttc cccgtatggt ctcagctgat cgaaggttat agccttgaag accccaaggc 900
 gaggcctcag gcgaaggggc tcgacagtgt gagccttcgc cactactgtg agcaggacct 960
 aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgttga 1020
 agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcac cgggtctcag 1080
 taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcacaa cagggtgcgtg 1140
 cgggtgtctc tcaggtaggg gactcgtttc ttagtgggtc tccagggtat gcagtcgatt 1200
 tgccatgccca tgccaaagga acctgttcca ggctcagtgc acctcaaac ccccgctcgt 1260
 ggaattgagc agtcggcgctc cgcctgtata gtacgactcg cctcggggcg cgtgttccga 1320
 agcaaaaagg tggtgggttc gttaccgaca acattgtatc ccacettgac attttacca 1380
 cctcttcccg ccgagaagca agcattggcg gaaaaatcta tccctggcta ctatagcaag 1440
 atagtctctg tatgggacaa ccdgtgggtg cgcgaaczag gctctctggg cgtctctcaa 1500
 tcgagctgtg accccatctc atttgcacga gataccagca tcgaagtcca tcggcaatgg 1560

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tccattacct gtttcattggt cggagaccgg ggacggaagt ggtcccaaca gtccaagcag 1620
gtaccgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaangc cggggcccaa 1680
gtcccagagc cggccaactg gctcgaaatc gactggctga agcagcagta ttccaagga 1740
gtcccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gtcagaacg 1800
ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa aggttatatg 1860
gaagggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctgggtgcca 1920
gcagcatag 1929

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<210> 36
<211> 600
<212> PRT
<213> Exophiala spinifera

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<400> 36

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1 5 10 15
Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240
Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260 265 270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290 295 300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

```

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 37
 <211> 1929
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)
 <221> intron
 <222> (1134)...(1186)

<400> 37
 atggcacttg cacagagcta catcaatccc ccaaagctcg cctccccagc aggggtattcc 60
 cacatcggcg taggccccaaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
 gacgcttttg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180
 ctgcgagcgt gccttgctgc agttaggagcc tcttcaaaag acgtcagcaa gctcaattac 240
 tacatcgctc actacgcccc gagcaaaact accgcaattg gagatgggct gaagtctacc 300
 tttgcccttg acaggctccc tctttgcaag ctgggtgccag taccggcctt ggccttcacct 360
 gaatacctct ttgaggttga cggcagggcg ctgggtgccag gacactcgac cccagacaaac 420
 gttgcggagc tggtagtggt gggcgctggc ttgagcggct tggagacggc accgaaagtc 480
 caggcgccgc gctctgctcg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
 ctgagcgtac aatcggttcc cggcaggagc actatcaacg acctcggcgc tgcgtggatc 600
 aatgacagca accaaagcga agtatccaga ttgcttgaaa gatttcattt ggagggcgag 660
 ctccagagga cgaccggaaa tccaatccat caagcacaag acggtacaac cactacagct 720

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ccttatgggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780
agaatacagt cactgactcc acttctgtcc gctgagcgag gaggttgcaa gtgcacttgc 840
ggaactccctc cccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggacct 960
aaacttgcct gctgttctca gogtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcga cgggtctcag 1080
taatatgttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
cggtgtctctc tcaggtaggg gactcgcttc ttagtgggtc ttcagggtat gcagtcgatt 1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgctcgt 1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggggc cgtgttccga 1320
agcaaaaagg tgggtggttc gttaccgaca acattgtatc ccactttgac attttcacca 1380
cctcttcccg ccgagaagca agcattggcg gaaaaatcta tctcggcta ctatagcaag 1440
atagtcttcg tatgggacaa cccgtgggtg cgcgaacaag gcttctcggg cgtctctcaa 1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcca tcggcaatgg 1560
tccattacct gtttcatggt cggagaccgg ggacggaggt ggtcccaaca gtccaagcag 1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cggggcccaa 1680
gtcccagagc cggccaacgt gctcgaaatc gactgggtcg agcagcagta tttccaagga 1740
gctccgagcg cgtctatggt gctgaacgat ctcacacac tgggttcggc gctcagaacg 1800
ccgttcaagt gtgttcattt cgttggaaac gagacgtctt tagtttggaa aggttatatg 1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctcgtgcga 1920
gcagcatag

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<210> 38
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

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<400> 38
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15
Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

```

```

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
      245      250      255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
      260      265      270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
      275      280      285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
      290      295      300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305      310      315      320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
      325      330      335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
      340      345      350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
      355      360      365
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370      375      380
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385      390      395      400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
      405      410      415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
      420      425      430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
      435      440      445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450      455      460
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465      470      475      480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      485      490      495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500      505      510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515      520      525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530      535      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545      550      555      560
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565      570      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580      585      590
Val Ala Ser Leu Val Pro Ala Ala
595      600

```

```

<210> 39
<211> 1930
<212> DNA
<213> Exophiala spinifera

```

```

<220>
<221> intron
<222> (739)...(811)

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<221> intron
<222> (1134)...(1187)

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<221> misc_feature
 <222> (648)...(648)
 <223> n = A,T,C or G

<400> 39

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gacgcttcgg gcgtagacaga ccttgccctac gagaaacagg ttggcccagg attcgccaat 180
ctgcgagctt gccttgctgc agttggagcc acttcaaacc acgtcaccaa gctcaattac 240
taccatcgtcg actacgcccc gagcaaacct accgcaattg gagatgggct gaaggctacc 300
tttgcctctg acaggctccc tctttgcacg ctgggtgcag tgtcggcctt gcttcacct 360
gaataacctt ttgaggttga tggcaccggcg ctgggtgcgg gacacacgac ccagacaaac 420
gttgcggagc tggtagtggg gggcgctggc ttgagcgtt tggagacggc acgcaaaagt 480
caggccggcg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
ctgagcgtac aatcggtgct cggcaggagc actatcaacg acctcggcgc tgcgtggatc 600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt gtagggcgag 660
ctccagagga cgattggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggt actccttggg aagcacaatc ccactttgtg atgagacctc tgtcagtggt 780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
ggaaactctc cccgtatggg ctccagctgat cgaagagcat agccttcaag acctcaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact 960
aaactttgct gctgttctcg gcgtagcaaa ccagatcaca cgcgtctctg tcggtgtgga 1020
agccccagag atcagcatgc ttttctcacg cgactacatc aagagtggca ccggtctcag 1080
taacttttct tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
tgggtctctc tcagggtggg gactcgttct tcaagtggtc atttcaggta tgcagtogat 1200
tggcaatgct alytcaaaag aacttgttcc aggcctcagt cactcctacc ccccgctgc 1260
tgaaattgag cagtcggcat cgggtctgtc agtacgatcg gcttcggggc ccgtgttccg 1320
aagcaaaaag gtggttgggt cgttaccgac aaccttgtat cccaccttga cattttcacc 1380
acctctcccc gccgagaagc aagcattggc ggaaaaattc atcctgggct actatagcaa 1440
gatagtcttc gtatgggaca agccttgggt gcgcgaacaa ggcttctcgg gcgtcctcca 1500
atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg 1560
gtccattacc tgtttcatgg tcggagaccc gggacgggag tggccccaac agtcccagca 1620
ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680
agtcocagag ccggcccaac tgctcgaaat ccagtggtcg aagcagcagt atttccaagg 1740
agctocgagc gccgtctatg ggtgaaacga tctcatcaca ctgggttcgg cgtcagaac 1800
gccgttcaag agtgttcatt tgcgttggaac ggagacgtct ttagtttgga aaggglatat 1860
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agcagcatag
  
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<210> 40
 <211> 598
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> VARIANT
 <222> (216)...(216)
 <223> Xaa = Any Amino Acid

<400> 40

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1      5      10      15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20     25     30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35     40     45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
  
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50						55						60					
Leu 65	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr		
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly		
			85						90					95			
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val		
			100					105					110				
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala		
		115					120					125					
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val		
			130			135					140						
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln		
145					150				155						160		
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly		
			165						170					175			
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn		
			180					185				190					
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser		
		195					200					205					
Arg	Leu	Phe	Glu	Arg	Phe	His	Xaa	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr		
		210				215					220						
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro		
225					230					235					240		
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu		
			245						250					255			
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp		
			260					265					270				
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala		
		275					280					285					
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Asn		
		290				295					300						
Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met		
305					310					315					320		
Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile		
			325						330					335			
Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly		
			340					345					350				
Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser		
		355					360					365					
Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly		
		370				375					380						
Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val		
385					390					395					400		
Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro		
			405														

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      515      520      525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
  530      535      540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
545      550      555      560
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
      565      570      575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
      580      585      590
Ser Leu Val Pro Ala Ala
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<210> 41
<211> 1928
<212> DNA
<213> Rhinocladiaella atrovirens

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<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1185)

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<400> 41

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gacgcttcgg ccgtgacaga cctgcctac gagaaacagg ttgccaagc attcgccaac 180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattacca gctcaattac 240
tacatcgctg actacaaccc gagcaaaccc accgcaattg gagatgggct gaaggctacc 300
tttgcccttg acaggctccc tcttgccag ctggtgccag tgcgggccct ggctccacct 360
gaataccctt ttgaggtga tgcacggcg ctggttccag gacactcaac cccagacaat 420
gttgcggacg tggctcgtgt gggcgctggc ctgagcggtt tggagacggc acgcaaagtc 480
caggctgcgg ggcgtgctct cctcgcttct gaggcgatgg atcgtgtggg gggaaagact 540
ctgagcgtac aatcgggtcc cggcaggagc gctatcaatg acctcgggcg tgcgtggatc 600
aatgacagca accaaagcga agtattcaaa ctatttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccggaaa ttcaatccat caagcacaa acggtacaac cactacagct 720
ccttatgggtg attccctggt aagcacaatt ccatcttggt atgagacctc tgtcgtgtgt 780
agaatacagt cgtgactcc acatcgcca gctgagcgag gaggttgcaa gtgcaactcg 840
ggaactcctt cccgcatggt ctgagctgat cgaagagcat agtcttgaag accccaaggc 900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960
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cgagctgtga ccccatctca ttgcccagag ataccagcat cgaagtcgat cggcaatggt 1560
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cgttcaaggg tgttcatttc gttggaacgg agacgtcttt gtttcggaaa gggatatgtg 1860
agggggccat acgatcgggt cagcgaggcg ctgcagaagt tggggttagc ctggtgccag 1920
cagcatag 1928

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<210> 42
 <211> 598
 <212> PRT
 <213> Rhinoclaadiella atrovirens

<400> 42

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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Ala
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35				40						45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
		50				55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Pro	Phe	Glu	Val	Asp	Ala
			115				120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
			130			135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Ala	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195				200						205			
Phe	Lys	Leu	Phe	Glu	Arg	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
		210				215						220			
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr
225					230					235				240	
Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu
			245						250					255	
Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro
		260						265					270		
Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His
		275				280						285			
Tyr	Cys	Glu	Lys	Asp	Leu	Ser	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn
		290				295					300				
Gln	Ile	Thr	Arg	Ala	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	
305					310					315				320	
Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile
			325						330					335	
Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly
			340					345					350		
Met	Gln	Ser	Leu	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser
		355					360					365			
Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly
		370				375					380				
Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Cys	Val
385					390					395				400	
Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro

405 410 415
 Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly
 420 425 430
 Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
 435 440 445
 Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
 450 455 460
 Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys
 465 470 475 480
 Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
 485 490 495
 Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn
 500 505 510
 Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
 515 520 525
 Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu
 530 535 540
 Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly
 545 550 555 560
 Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
 565 570 575
 Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
 580 585 590
 Ser Leu Val Pro Ala Ala
 595

<210> 43
 <211> 1928
 <212> DNA
 <213> *Rhinocladiaella atrovirens*

<220>
 <221> intron
 <222> (739)...(811)
 <221> intron
 <222> (1134)...(1186)

<400> 43

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gacgcttcgg	cctgacaga	ccttgctac	gagaaacagg	ttgcccagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agtgaggcc	acttcaaacg	acattaccaa	gtcgaattac	240
tacatcgctg	actacaaccc	gagcaactc	acgcgaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgccggccct	ggcttcaact	360
gaatacctct	ttgaggttga	tgccacggcg	ctgggttccag	gacactcaac	cccagacaat	420
gttaccgacg	tggctcgtgt	ggcgctggc	ctggaggggt	tggagacggc	acgcaaaagtc	480
caggctgcgg	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgctgg	gggaaagact	540
ctgagcgta	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tcgctggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	attccctggt	aagcacaatt	ccatctctgt	atgagacctc	tgctgtgtgt	780
agaatacagt	cgtgactcc	acatcgtcca	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	cccgcatggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgc	gagcttcgca	cactactgtg	agaaggact	960
aaacttgctt	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgt	ctttctctac	cgactacatc	aagagtgcct	ccggtctcag	1080
taatatgtgc	tcggataaga	aagacggctg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140

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tgggtgtctc tcagtgggag actcgtttct tagtgggtcat tccaggtatg cagtcgtttt 1200
gccatgccat gtcaaaggaa cttgtttccag gctcagtgcg cctcaacacc cccgtcgccg 1260
aaattgagca gtcggcater ggctgtacag tacgatgggc ctgggggggc gtgttccgaa 1320
gtaaaaagggt gggtgtttcg ttaccgacaa ccttgtatcc caccttgata ttttcaccac 1380
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tagctttcgt atgggacaa gctgtgtggc gogaacaagg cttctcgggc gtccccaat 1500
cgagctgtga ccccatctca ttgtccagag ataccagcat cgaagtccat cggcaatggg 1560
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cgttcaagggt tgttcatttc gttggaacgg agacgtcttt ggtttgaaa ggttatatgg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctgggtgccg 1920
cagcatag 1928

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<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
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Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180 185 190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195 200 205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225 230 235 240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245 250 255
Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260 265 270
Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
275 280 285
Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg

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290 295 300
 Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
 305 310 315 320
 Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
 325 330 335
 Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
 340 345 350
 Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
 355 360 365
 Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
 370 375 380
 Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
 385 390 395 400
 Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 405 410 415
 Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 420 425 430
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 435 440 445
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
 450 455 460
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 465 470 475 480
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 485 490 495
 Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 500 505 510
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 515 520 525
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
 545 550 555 560
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 565 570 575
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 580 585 590

<210> 45
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)
 <221> intron
 <222> (1134)...(1185)

<400> 45
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 gagcttcgg ccgtgacaga cctgcctac gagaaacagg ttgcccagc attcggcaac 180
 ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccac gctcaattac 240
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 ttgtcccttg ataggctccc tcttgcaag ctggtgcccag tgcgggcccct ggtttcacct 360
 gaataacctt ctgaggttga tgctacggcg ctggttccag gacactcaac ccagagcaat 420

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gttgoggagc tgggtcgtgtt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480
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ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc 600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccgggaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggtg attccctgtt aggcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780
agaatacagt cgtgactcc acatcgcca gctgagcgag saggttgcaa gtgcactcgc 840
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gagccctcaa gcaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960
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agccacagag atcagcatgc tttttctcac cgactacatc aagagtgcga ccggtctcag 1080
taatatgttc tcggataaga aagacgggtg gcagtatatg cgatgcaaaa caggtgcgtg 1140
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cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1920
cagcatag

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<210> 46

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 46

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20      25      30
Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35      40      45
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50      55      60
Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65      70      75      80
Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85      90      95
Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100     105     110
Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115     120     125
Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130     135     140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145     150     155     160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165     170     175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180     185     190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe

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80

195 200 205
 Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
 210 215 220
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
 225 230 235 240
 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
 245 250 255
 Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
 260 265 270
 Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
 275 280 285
 His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
 290 295 300
 Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
 305 310 315 320
 Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
 325 330 335
 Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
 340 345 350
 Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
 355 360 365
 Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
 370 375 380
 Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
 385 390 395 400
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
 405 410 415
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
 420 425 430
 Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
 435 440 445
 Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
 450 455 460
 Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
 465 470 475 480
 Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
 485 490 495
 Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
 500 505 510
 Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
 515 520 525
 Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
 545 550 555 560
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 565 570 575
 Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
 580 585 590

<210> 47

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 47

~~Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro~~
 1 3 10 15

81

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270
 Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
 420 425 430
 Leu Gly Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

```

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      485      490      495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
      500      505      510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
      515      520      525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
      530      535      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545      550      555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
      560      565      570      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
      580      585      590
Val Ala Ser Leu Val Pro Ala Ala
      595      600

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<210> 48
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

```

<400> 48
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gcc ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
  1          5          10          15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20          25          30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg      144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45

ggt ccc ggc agg acg act atc aac gac ctc ggc gcc gcg tgg atc aat      192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50          55          60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
          65          70          75          80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100          105          110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg cct cag ctg      384
          83

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Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc gcc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac gcc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc gcc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Gln Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	

```

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
      355                      360                      365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
      370                      375                      380

ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
      385                      390                      395                      400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
      405                      410                      415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
      420                      425                      430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1346
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
      435                      440                      445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
      450                      455                      460

```

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1          5          10          15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
      20          25          30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
      35          40          45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
      50          55          60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
      65          70          75          80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
      85          90          95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
      100          105          110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
      115          120          125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
      130          135          140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
      85

```

```

145          150          155          160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
          165          170          175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
          180          185          190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
          195          200          205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
          210          215          220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
          225          230          235          240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
          245          250          255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
          260          265          270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
          275          280          285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
          290          295          300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
          305          310          315          320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
          355          360          365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
          385          390          395          400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

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<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50

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aaa gac aac gtt gcg gac ggg gta ggg ggg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5          10          15

```

```

----- ttg gag acg gca cgc aaa gtc cag gcc gcc ggt cag tcc tgc ctc gtc ----- 96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

```

86

20	25	30	
ctt gag ggc atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45			144
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 55 70 75 80			240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt ggc gaa ctc ctc ccc gta tgg tot cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768

```

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc      815
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                260                265                270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                275                280                285

gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc      912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
                290                295                300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tgc gcc gtc ctc      960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
                305                310                315                320

caa tgc agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac      1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                330                335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga      1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340                345                350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                355                360                365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
                370                375                380

ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
                385                390                395                400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                410                415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                420                425                430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                435                440                445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
                450                455                460

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<210> 51

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 52

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctg gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctg gcc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag gcc gag ctg cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctg ctg ccc gta tgg tct cag ctg 384
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125

atc gaa gag cat agc ctt caa gac ctg aag gcg agc cct cag gcg aag 432
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140

cgg ctg gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtc cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtc tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	

```

385          390          395          400
gga gcc ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acc gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445

caa cga ggt gct gca gaa gtt gtg gcc agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
          450          455          460

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<210> 53
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

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<400> 53
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1          5          10          15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
          20          25          30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50          55          60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
          65          70          75          80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100          105          110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
          115          120          125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
          130          135          140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
          145          150          155          160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
          165          170          175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
          180          185          190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
          195          200          205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
          210          215          220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
          92

```

```

225          230          235          240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
          245          250          255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
          260          265          270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
          275          280          285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
          290          295          300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305          310          315          320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350
Arg Lys Trp Ser Gln Gln Ser Lys Lys Val Arg Gln Lys Ser Val Trp
          355          360          365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385          390          395          400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

```

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<210> 54
<211> 8
<212> PRT
<213> Unknown

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<220>
<223> Artificial Sequence

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<400> 54

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Gly Gly Gly Ser Gly Gly Gly Ser
1          5

```

```

<210> 55
<211> 11
<212> PRT
<213> Exophilal spinifera

```

```

<400> 55

```

```

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5          10

```